

09786635 Results

SEQ ID NO: 1

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	6880	100.0	6880	6	AX253450	AX253450 Sequence
2	6880	100.0	6880	9	HSA012376	AJ012376 Homo sapi
3	6880	100.0	7260	6	AX253452	AX253452 Sequence
4	6879	100.0	9497	6	AX059973	AX059973 Sequence
5	6879	100.0	9497	9	AF165281	AF165281 Homo sapi
6	6875.8	99.9	9741	6	AX127830	AX127830 Sequence
7	6875.8	99.9	9741	6	AX139817	AX139817 Sequence
8	6875.8	99.9	9741	6	AX351038	AX351038 Sequence
9	6875.8	99.9	9854	6	AX127831	AX127831 Sequence
10	6875.8	99.9	9854	6	AX139818	AX139818 Sequence
11	6870.4	99.9	7860	6	AX092594	AX092594 Sequence
12	6865	99.8	9495	6	AX059978	AX059978 Sequence
13	6862.4	99.7	10442	6	AX060713	AX060713 Sequence
14	6862.4	99.7	10442	6	AX060892	AX060892 Sequence
15	6862.4	99.7	10442	9	AF285167	AF285167 Homo sapi
16	6860.8	99.7	10474	6	AX060719	AX060719 Sequence
17	6860.8	99.7	10474	6	AX060721	AX060721 Sequence
18	6860.8	99.7	10474	6	AX060898	AX060898 Sequence
19	6860.8	99.7	10474	6	AX060900	AX060900 Sequence
20	6845.2	99.5	7862	6	AX135712	AX135712 Sequence
21	6760.2	98.3	9593	6	AX059976	AX059976 Sequence
22	6711.6	97.6	6786	9	AB055982	AB055982 Homo sapi
23	5630	81.8	7878	10	MMABC1	X75926 Mus musculu
24	5455.6	79.3	6801	10	AY208182	AY208182 Rattus no
25	4302	62.5	7074	5	AF362377	AF362377 Gallus ga
26	2052.4	29.8	5097	6	BD012346	BD012346 Genes rel
27	2052.4	29.8	5097	6	BD160225	BD160225 Primer fo
28	2052.4	29.8	5097	9	AK027864	AK027864 Homo sapi
29	1911.6	27.8	7298	9	AF001945	AF001945 Homo sapi

AF165281

LOCUS AF165281 9497 bp mRNA linear PRI 17-AUG-1999

DEFINITION Homo sapiens ATP cassette binding transporter 1 (ABC1) mRNA, complete cds.

ACCESSION AF165281

VERSION AF165281.1 GI:5734100

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 9497)

AUTHORS Rust,S., Rosier,M., Funke,H., Real,J., Amoura,Z., Piette,J.C., Deleuze,J.F., Brewer,H.B., Duverger,N., Deneffe,P. and Assmann,G.

TITLE Tangier disease is caused by mutations in the gene encoding ATP-binding cassette transporter 1

JOURNAL Nat. Genet. 22 (4), 352-355 (1999)

MEDLINE 99364413

PUBMED 10431238

REFERENCE 2 (bases 1 to 9497)

AUTHORS Rust,S., Rosier,M., Funke,H., Real,J., Amoura,Z., Piette,J.C., Deleuze,J.F., Brewer,H.B., Duverger,N., Deneffe,P. and Assmann,G.

TITLE Direct Submission

JOURNAL Submitted (01-JUL-1999) Genomics, Rhone-Poulenc Rorer, 2 rue Gaston Cr#mieux, Evry 91006, France

FEATURES Location/Qualifiers

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/organism="Homo sapiens"

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ORIGIN

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Query Match      100.0%; Score 6879; DB 9; Length 9497;
Best Local Similarity 100.0%; Pred. No. 0;
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Db    121 ATGCCCTCTGCAGGAACACTTCCTTGGGTTTCAGGGGATTATCTGTAATGCCAACAACCCC 180

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Qy	361	AACTTGAAGCTTCAAGATTTCTGGTGGACAATGAAACCTTCTCTGGGTTCTGTATCAC	420
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Qy	481	AAGGTATTTTTGCAAGGCTACCAGTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA	540
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Qy	661	AGAACTAACTCTACATCTCCCTTCCCGAGCAAGGAGCTGGCCGAAGCCACAAAAACA	720
Db	661	AGAACTAACTCTACATCTCCCTTCCCGAGCAAGGAGCTGGCCGAAGCCACAAAAACA	720
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Qy	781	ATGCGACAGGAGGTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCCTCCACCCAAATC	840
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Qy	901	TCTCTCAACTGGTATGAGGACAACAACCTACAAGCCCTCTTTGGAGGCAATGGCACTGAG	960
Db	901	TCTCTCAACTGGTATGAGGACAACAACCTACAAGCCCTCTTTGGAGGCAATGGCACTGAG	960
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Db	1021	AATTTGGAGTCTAGTCTCTTTCCCGCATTATCTGGAAAGCTCTGAAGCCGCTGCTCGTT	1080
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Db	1081	GGGAAGATCCTGTATACACCTGACACTCCAGCCACAAGGCAGGTCAATGGCTGAGGTGAAC	1140
Qy	1141	AAGACCTTCCAGGAACTGGCTGTGTTCCATGATCTGGAAGGCATGTGGGAGGAACTCAGC	1200
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Qy	1321	CAAGACATCGTGGCGTTTGGCCAAGCACCAGAGGATGTCCAGTCCAGTAATGGTTCT	1380
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Qy	1681	GACCCCTTTGAGGACATGCGGTACGTCTGGGGGGGCTTCGCCTACTTGCAGGATGTGGTG	1740
Db	1681	GACCCCTTTGAGGACATGCGGTACGTCTGGGGGGGCTTCGCCTACTTGCAGGATGTGGTG	1740
Qy	1741	GAGCAGGCAATCATCAGGGTGTGACGGGCACCGAGAAGAAAACTGGTGTCTATATGCAA	1800
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Db	1981	CTCTGGTTTAGCTGGTTTCATTAGTAGCCTCATTCCTCTTCTGTGAGCGCTGGCCTGCTA	2040
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Qy	2101	TTCTGTCCGTGTTTGCTGTGGTGACAAATCCTGCAGTGCTTCCTGATTAGCACACTCTTC	2160
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Qy	2161	TCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTACCTGCCC	2220
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Db	4441	 ACAGGAAGAAACATTTTCGGATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGC	4500
Qy	4501	TTAAAGAACAAAGATCTGGGTGAATGAGTTTAGGTATGGCGGCTTTTCCTGGGTGTCAGT	4560
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Qy	4561	AATACTCAAGCACTTCCTCCGAGTCAAGAAGTTAATGATGCCACCAACAAATGAAGAAA	4620
Db	4561	AATACTCAAGCACTTCCTCCGAGTCAAGAAGTTAATGATGCCACCAACAAATGAAGAAA	4620
Qy	4621	CACCTAAAGCTGGCCAAGGACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTT	4680
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Qy	4801	GGAGAGAACCCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAG	4860
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Qy	4981	GTCAGCAAAGCAAAACACCTGCAGTTTCATCAGTGGAGTGAAGCCTGTCTACTGGGCTC	5040
Db	4981	GTCAGCAAAGCAAAACACCTGCAGTTTCATCAGTGGAGTGAAGCCTGTCTACTGGGCTC	5040
Qy	5041	TCTAATTTTGTCTGGGATATGTGCAATTACGTTGTCCCTGCCACACTGGTCATTATCATC	5100
Db	5041	TCTAATTTTGTCTGGGATATGTGCAATTACGTTGTCCCTGCCACACTGGTCATTATCATC	5100
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Db	5401	GACATGGTGAAAAACAGGCAATGGCTGATGCCCTGGAAAGGTTTGGGGAGAATCGCTTT	5460
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Qy	5521	GTGGTGTTCCTCCTCATTACTGTTCTGATCCAGTACAGATTCTTCATCAGGCCAGACCT	5580
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Qy	6301	AGGTTCAAGGTGCCTTGGCAGTGTCCAGCATCTAAAAAATAGGTTTGGAGATGGTTATACA	6360
Db	6301	AGGTTCAAGGTGCCTTGGCAGTGTCCAGCATCTAAAAAATAGGTTTGGAGATGGTTATACA	6360
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Db	6421	CTTGCAATTTCTGGAAGTGTTCAAAAGAGAAACACCGGAACATGCTACAATACCAGCTT	6480
Qy	6481	CCATCTTCATTATCTTCTCTGGCCAGGATATTTCAGCATCCTCTCCAGAGCAAAAAGCGA	6540
Db	6481	CCATCTTCATTATCTTCTCTGGCCAGGATATTTCAGCATCCTCTCCAGAGCAAAAAGCGA	6540
Qy	6541	CTCCACATAGAAGACTACTCTGTTTCTCAGACAACACTTGACCAAGTATTTGTGAACTTT	6600
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SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	6880	100.0	6880	21	AAZ94734	Human ATP binding
2	6880	100.0	6880	22	AAI70314	Human ATP binding
3	6880	100.0	7260	22	AAD21326	Human ATP binding
4	6880	100.0	7260	22	AAI70315	Human ATP binding
5	6879	100.0	9497	24	ABV78020	Hypoxia-regulated
6	6876.8	100.0	6880	22	AAD21325	Human ATP binding
7	6875.8	99.9	9741	22	AAS06120	Human ABC1 DNA seq
8	6875.8	99.9	9741	24	AAD37273	Human ABC1 full-le
9	6875.8	99.9	9854	22	AAS06121	Human ABC1 DNA seq
10	6875.8	99.9	9870	24	ABN99301	Polymorphic human
11	6875.8	99.9	9870	24	ABN99302	Polymorphic human
12	6875.8	99.9	9870	24	ABN99303	Polymorphic human
13	6875.8	99.9	9870	24	ABN99324	Polymorphic human
14	6875.8	99.9	9870	24	ABN99328	Polymorphic human
15	6875.8	99.9	9870	24	ABN99329	Polymorphic human
16	6875.8	99.9	9870	24	ABN99330	Polymorphic human
17	6875.8	99.9	9870	24	ABN99331	Polymorphic human
18	6875.8	99.9	9870	24	ABN99332	Polymorphic human
19	6875.8	99.9	9870	24	ABN99333	Polymorphic human
20	6875.8	99.9	9870	24	ABN99334	Polymorphic human
21	6875.8	99.9	9870	24	ABN99335	Polymorphic human
22	6875.2	99.9	7281	22	AAK51683	Human polynucleoti
23	6874.2	99.9	9741	24	ABL58146	Human ABCA1 transp
24	6874.2	99.9	9870	24	ABN99304	Polymorphic human
25	6874.2	99.9	9870	24	ABN99305	Polymorphic human
26	6874.2	99.9	9870	24	ABN99306	Polymorphic human
27	6874.2	99.9	9870	24	ABN99307	Polymorphic human
28	6874.2	99.9	9870	24	ABN99309	Polymorphic human
29	6874.2	99.9	9870	24	ABN99310	Polymorphic human
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36	6874.2	99.9	9870	24	ABN99317	Polymorphic human
37	6874.2	99.9	9870	24	ABN99318	Polymorphic human
38	6874.2	99.9	9870	24	ABN99319	Polymorphic human
39	6874.2	99.9	9870	24	ABN99320	Polymorphic human
40	6874.2	99.9	9870	24	ABN99321	Polymorphic human
41	6874.2	99.9	9870	24	ABN99322	Polymorphic human
42	6874.2	99.9	9870	24	ABN99323	Polymorphic human
43	6874.2	99.9	9870	24	ABN99325	Polymorphic human
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45 6874.2 99.9 9870 24 ABN99327

Polymorphic human

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	430.8	6.3	5894	3	US-08-665-259-24	Sequence 24, Appl
2	430.8	6.3	5894	3	US-08-762-500-24	Sequence 24, Appl
3	430.8	6.3	6525	3	US-08-762-500-74	Sequence 74, Appl
4	99.4	1.4	1008	4	US-09-252-991A-4266	Sequence 4266, Ap
c 5	98.8	1.4	999	4	US-09-252-991A-4588	Sequence 4588, Ap
6	89.4	1.3	1614	4	US-09-252-991A-4198	Sequence 4198, Ap
7	85.8	1.2	1824	4	US-09-252-991A-1780	Sequence 1780, Ap
8	83.8	1.2	1176	4	US-09-252-991A-3704	Sequence 3704, Ap
c 9	83.8	1.2	2253	4	US-09-252-991A-3810	Sequence 3810, Ap
10	81	1.2	36181	4	US-08-311-731A-120	Sequence 120, App
11	78.4	1.1	1548	4	US-09-252-991A-3653	Sequence 3653, Ap
c 12	77.4	1.1	762	4	US-09-252-991A-1938	Sequence 1938, Ap
c 13	76.6	1.1	4411529	3	US-09-103-840A-1	Sequence 1, Appli
14	75.2	1.1	969	4	US-09-107-532A-1008	Sequence 1008, Ap
15	75	1.1	1770	4	US-09-328-352-3466	Sequence 3466, Ap

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	3600.4	52.3	4783	11	AK051920	AK051920 Mus muscu
2	1024.8	14.9	3605	11	AK052916	AK052916 Mus muscu
3	692.4	10.1	809	12	BI754756	BI754756 603025477
4	636.6	9.3	854	12	BI854140	BI854140 603381449
5	624.4	9.1	754	14	CD351847	CD351847 UI-M-GIO-
c 6	591.2	8.6	878	12	BI182779	BI182779 UNL-P-FN-
7	587.8	8.5	673	14	CD351490	CD351490 UI-M-GIO-
c 8	550.4	8.0	661	14	CB481810	CB481810 jns83_A02
9	547.6	8.0	773	14	CB526974	CB526974 UI-M-FY0-
10	542	7.9	837	10	BF160011	BF160011 601768192
11	536.8	7.8	652	10	BB468374	BB468374 BB468374
12	535.2	7.8	702	12	BI658600	BI658600 603284335
13	532.4	7.7	724	12	BG920223	BG920223 602822304
c 14	528.4	7.7	639	14	CB477340	CB477340 jns20_C11
15	525	7.6	720	12	BI248317	BI248317 602966918
16	516	7.5	620	14	CA889361	CA889361 B0152D10-
17	510.4	7.4	512	13	BX279856	BX279856 BX279856
c 18	505	7.3	614	14	CB478239	CB478239 jns32_B02
19	486.4	7.1	605	14	CB546553	CB546553 AMGNNUC:N
20	479.8	7.0	579	14	CA884367	CA884367 B0109G01-
21	477	6.9	1004	11	BC034824	BC034824 Homo sapi
22	473	6.9	562	10	BE665489	BE665489 154542 MA
23	459.4	6.7	515	10	BF094524	BF094524 MR0-UT004
24	456.8	6.6	605	14	CB581583	CB581583 AMGNNUC:N
25	447.6	6.5	554	10	BF076322	BF076322 225856 MA
26	438.4	6.4	512	14	CB717058	CB717058 AMGNNUC:N
27	435.6	6.3	884	13	BU906084	BU906084 AGENCOURT

RESULT 1

AK051920

LOCUS AK051920 4783 bp mRNA linear HTC 05-DEC-2002

DEFINITION Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length enriched library, clone:D230019D04 product:ATP-binding cassette, sub-family A (ABC1), member 1, full insert sequence.

ACCESSION AK051920

VERSION AK051920.1 GI:26342297

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636

REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159

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AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
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Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
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TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861

REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
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Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
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Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
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TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851

REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 4783)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
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Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
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Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,

Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

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GGNTEEDVDTFYDNSTTPYCNDLMKNLESSPLSRIIWKALKPLLVGKILYTPDTPAT
RQVMAEVNKTQELAVFHLEGMWEELSPQIWTFMENSQEMDLVRTLLDSRGNDQFWE
QKLDGLDWTQDIMAFLAKNPEDAQSPNGSVYTWREAFNETNQAIQTISRFMECVNLN
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PCYVDDIFLRVMSRSMPLFMTLAWIYSVAVIKSIYVEKEARLKETMRIMGLDNGILW
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EQGIGVQWQDNLFESPVEEDGFNLTTAVSMMLFDTFLYGVMTWYIEAVFPQGYGIPRPW
YFPCTKSYWFGEEIDEXSHPGSSQKGVSEICMEEEPHTHLRQVSIQNLVKVYRDGMKV
AVDGLALNFYEGQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYILGKDIRSEMSSIR
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BASE COUNT 1119 a 1236 c 1310 g 1118 t

ORIGIN

Query Match 52.3%; Score 3600.4; DB 11; Length 4783;
Best Local Similarity 88.6%; Pred. No. 0;
Matches 3901; Conservative 0; Mismatches 501; Indels 0; Gaps 0;

Qy 1 CAAACATGTCAGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCTGATCCTGATC 60

Db	382	CAAAACATGTCAGCTGTTACTGGAAGTGGCCTGGCCTCTCTTTATCTTCCTGATCCTGATC	441
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Db	442	TCTGTACGCCTGAGCTACCCACCCTACGAACAACATGAGTGCCACTTTCCGAATAAAGCC	501
Qy	121	ATGCCCTCTGCAGGAACACTTCCTTGGGTTACAGGGATTATCTGTAATGCCAACAAACCCC	180
Db	502	ATGCCGTCTGCAGGAACCTCCCTGGGTACAGGGATTATCTGTAATGCCAACAAACCCC	561
Qy	181	TGTTTTCCGTTACCCGACTCCTGGGGAGGCTCCCGAGTTGTTGGAACTTTAACAATCC	240
Db	562	TGCTTCCGTTATCCAACCTCCCGCGAGGCTCCCGGTGTTGTTGGAACTTTAACAAGTCC	621
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Db	622	ATCGTGTCTCGCCTGTTCTCAGACGCTCAGAGGCTTCTTCTGTACAGCCAAAGAGATACC	681
Qy	301	AGCATGAAGGACATGCGCAAAGTTCTGAGAACATTACAGCAGATCAAGAAATCCAGCTCA	360
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Qy	361	AACTTGAAGCTTCAAGATTTCTGGTGGACAATGAAACCTTCTCTGGGTTCTGTATCAC	420
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Qy	421	AACCTCTCTCTCCCAAAGTCTACTGTGGACAAGATGCTGAGGGCTGATGTCAATTCTCCAC	480
Db	802	AATTTGTCCCTTCCAAGATCTACTGTGGACAGCCTGCTGCAGGCGAATGTTGGTCTCCAG	861
Qy	481	AAGGTATTTTTGCAAGGCTACCAGTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA	540
Db	862	AAGGTATTTTTGCAAGGCTACCAATTACATTTGGCCAGTCTGTGTAACGGATCAAAATTA	921
Qy	541	GAAGAGATGATTCAACTTGGTGACCAAGAAGTTTCTGAGCTTTGTGGCCTACCAAGGGAG	600
Db	922	GAAGAAATTATTTCAGCTTGGTGATGCGGAAGTTTCTGCCCTCTGTGGTCTACCGAGGAAG	981
Qy	601	AAACTGGCTGCAGCAGAGCGAGTACTTCGTTCCAACATGGACATCCTGAAGCCAATCCTG	660
Db	982	AAGCTCGATGCAGCCGAGAGTACTGCGCTACAACATGGACATCCTGAAGCCAGTTGTG	1041
Qy	661	AGAACTAACTAACTCTACATCTCCCTTCCCGAGCAAGGAGCTGGCCGAAGCCACAAAAACA	720
Db	1042	ACAAAACATAAATTCCACATCTCATCTCCCGACCCAGCATCTGGCTGAAGCCACCACAGTG	1101
Qy	721	TTGCTGCATAGTCTTGGGACTCTGGCCCAGGAGCTGTTTACGATGAGAAGCTGGAGTGAC	780
Db	1102	TTGCTTGACAGCTTGGGGGCCCTGGCCCAAGAGCTGTTTACGACAAAGAGCTGGAGCGAC	1161
Qy	781	ATGCGACAGGAGGTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCCTCCACCCAAATC	840
Db	1162	ATGCGGCAGGAGGTGATGTTTCTGACCAACGTGAACAGCTCCAGCTCCTCCACCCAGATC	1221
Qy	841	TACCAGGCTGTGTCTCGTATTGTCTGCGGGCATCCCGAGGGAGGGGGCTGAAGATCAAG	900
Db	1222	TACCAGGCAGTGTCCCGCATCGTGTGTGGTACCCAGAGGGTGGGGCTGAAGATCAAG	1281
Qy	901	TCTCTCAACTGGTATGAGGACAACAATAACAAGCCCTCTTTGGAGGCAATGGCACTGAG	960
Db	1282	TCCCTCAACTGGTACGAGGATAACAATAACAAGCCCTCTTTGGAGGGAATAACACCGAG	1341
Qy	961	GAAGATGTGAAACCTTCTATGACAACCTTCACTGCAATGATTTGATGAAG	1020
Db	1342	GAAGACGTGGACACCTTCTATGACAATCTTCACTGCAATGATTTGATGAAG	1401
Qy	1021	AATTTGGAGTCTAGTCTCTTTTCCCGCATTATCTGGAAAGCTCTGAAGCCGCTGCTCGTT	1080
Db	1402	AACCTGGAGTCTAGTCTCTTTTCTCGAATTATTGGAAGGCACTCAAGCCACTGCTTGTT	1461

Qy	1081	GGGAAGATCCTGTATACACCTGACACTCCAGCCACAAGGCAGGTCATGGCTGAGGTGAAC	1140
Db	1462	GGAAAGATTCTCTATACACCTGACACACCAGCTACAAGGCAGGTCATGGCTGAGGTGAAC	1521
Qy	1141	AAGACCTTCCAGGAACCTGGCTGTGTTCCATGATCTGGAAGGCATGTGGGAGGAACTCAGC	1200
Db	1522	AAGACCTTTCAGGAGTTGGCTGTGTTCCATGACCTGGAGGGCATGTGGGAAGAACTCAGC	1581
Qy	1201	CCCAAGATCTGGACCTTCATGGAGAACAGCCAAGAAATGGACCTTGTCGGGATGCTGTTG	1260
Db	1582	CCCCAAATTTGGACCTTCATGGAGAACAGCCAAGAGATGGACCTTGTCGGGACGCTGTTA	1641
Qy	1261	GACAGCAGGGACAATGACCACTTTTGGGAACAGCAGTTGGATGGCTTAGATTGGACAGCC	1320
Db	1642	GACAGCAGAGGCAATGACCACTTTTGGGAACAGAAAGTTGGATGGATTAGATTGGACTGCC	1701
Qy	1321	CAAGACATCGTGGCGTTTCTGGCCAAGCACCAGAGGATGTCCAGTCCAGTAATGGTTCT	1380
Db	1702	CAAGACATCATGGCGTTTCTGGCCAAGAACCCAGAAGATGCTCAGTCCCCAAATGGCTCT	1761
Qy	1381	GTGTACACCTGGAGAGAAGCTTTCAACGAGACTAACCGGCAATCCGGACCATATCTCGC	1440
Db	1762	GTGTATACCTGGAGAGAAGCTTTCAATGAGACCAACCGGCAATCCAGACGATATCTCGA	1821
Qy	1441	TTCATGGAGTGTGTCAACCTGAACAAGCTAGAACCCATAGCAACAGAAGTCTGGCTCATC	1500
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Qy	1501	AACAAGTCCATGGAGCTGCTGGATGAGAGGAAGTTCTGGGCTGGTATTGTGTTCACTGGA	1560
Db	1882	AACAAGTCCATGGAGCTGCTGGACGAGAGGAAGTTCTGGGCTGGCATCGTGTTCACAGGC	1941
Qy	1561	ATTACTCCAGGCAATGAGCTGCCCCATCATGTCAAGTACAAGATCCGAATGGACATT	1620
Db	1942	ATCACTCCAGATAGTGTGGAGCTGCCCCATCATGTAAAGTACAAGATCCGGATGGACATT	2001
Qy	1621	GACAAATGTGGAGAGGACAATAAAATCAAGGATGGGTACTGGGACCTGGTCTCGAGCT	1680
Db	2002	GACAACGTGGAGAGAACTAATAAGATCAAGGATGGGTACTGGGACCTGGTCTCGGGCT	2061
Qy	1681	GACCCCTTTGAGGACATGCGGTACGTCTGGGGGGGCTTCGCCTACTTGACAGGATGTGGTG	1740
Db	2062	GACCCCTTTTGAAGATATGCGCTATGTCTGGGGCGGCTTCGCCTACTTGACAGGATGTGGTG	2121
Qy	1741	GAGCAGGCAATCATCAGGGTGCTGACGGGCACCGAGAAGAAAACCTGGTGTCTATATGCAA	1800
Db	2122	GAAACAGGCCATCATCAGAGTGCTGACGGGATCTGAGAAGAAAACGGGTGTCTACGTGCAA	2181
Qy	1801	CAGATGCCCTATCCCTGTTACGTTGATGACATCTTTCTGCGGGTGATGAGCCGGTCAATG	1860
Db	2182	CAGATGCCCTACCCCTGTTATGTTGATGACATTTTTCTGCGGGTCATGAGCCGGTCAATG	2241
Qy	1861	CCCCCTTTCATGACGCTGGCCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCATCGTG	1920
Db	2242	CCCCCTTTCATGACTCTAGCCTGGATCTACTCTGTCTGCTGTGATCATCAAGAGCATTGTG	2301
Qy	1921	TATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATCATGGGCCTGGACAACAGCATC	1980
Db	2302	TATGAGAAGGAGGCTCGGCTGAAGGAGACCATGCGGATCATGGGTCTGGACAATGGCATC	2361
Qy	1981	CTCTGGTTTAGCTGGTTCAATTAGTAGCCTATTCTCTTCTTGAGCGCTGGCCTGCTA	2040
Db	2362	CTCTGGTTTAGCTGGTTTGTAGTAGCCTCATCCCTCTGCTTGAGCGCTGGCCTGCTG	2421
Qy	2041	GTGGTCATCTTGAAGTTAGGAAACCTGTGCGCTACAGTGATCCAGCGTGGTGTTCGTC	2100
Db	2422	GTGGTCATCTTGAAGTTAGGAAACCTGTGCGCTATAGTGACCCAGCGTGGTGTTCGTC	2481
Qy	2101	TTCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGCTTCCTGATTAGCAGCTCTTC	2160
Db	2482	TTCTGTCTGTGTTTGCCATGGTGACCATCCTACAGTGCTTCCTCATTAGCAGCTCTTC	2541

Qy	2161	TCCAGAGCCCAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTACCTGCCC	2220
Db	2542		2601
Qy	2221	TACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGC	2280
Db	2602		2661
Qy	2281	CTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCCCCTTTTGGAGGAGCAG	2340
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Qy	2341	GGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCTGTGGAGGAAGATGGCTTCAAT	2400
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Qy	2401	GGTATCGGGGTCCAATGGGACAATCTCTTTGAGAGCCCGGTGGAGGAGGACGGCTTCAAT	2460
Db	2782		2841
Qy	2461	CTCACCACTTCGGTCTCCATGATGCTGTTTGACACCTTCCTCTATGGGGTGATGACCTGG	2520
Db	2842		2901
Qy	2521	TACATCGAAGCCGTCTTTCCAGGACAGTATGGAATTCCCAGGCCCTGGTATTTTCTTGT	2580
Db	2902		2961
Qy	2581	ACCAAGTCCTACTGGTTTGGCGAGGAAAGTGATGAGAAGAGCCACCTGGTTCCAACCAG	2640
Db	2962		3021
Qy	2641	AAGGAGTGTCAGAAATCTGCATGGAAGAGGAACCCACTCATCTGAGGCTGGGGGTGTC	2700
Db	3022		3081
Qy	2701	ATTTCAGAACCTGGTAAAGTCTACCGAGATGGGATGAAGGTGGCTGTGATGGCCTGGCA	2760
Db	3082		3141
Qy	2761	CTCAACTTTTACGAAGGCCAGATTACCTCCTTCTGGGCCACAATGGAGCAGGGAAGACC	2820
Db	3142		3201
Qy	2821	ACCACCATGTCAATCCTGACCGGGTGTTCCCCCCGACCTCGGGCACCGCCTACATCCTG	2880
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Qy	2881	GGGAAAGACATTGCTCGGAGATGAGCTCCATCCGGCAGAACCTGGGAGTCTGTCCCCAG	2940
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Qy	2941	CATAACGTGCTGTTTGACATGCTGACTGTCGAAGAACACATCTGGTTCTATGCCCCGCTTG	3000
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Qy	3001	AAGGGGCTCTCAGAGAAGCACGTAAGGCGGAGATGGAGCAGATGGCCCTGGATGTTGGT	3060
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Qy	3061	TTGCCATCAAGCAAGCTGAAAAGCAAAACAAGCCAGCTGTGAGGTGGAATGCAGAGAAAAG	3120
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Qy	3121	CTATCTGTGGCCTTGGCCTTTGTGCGGGGATCTAAGGTTGTCAATTCTGGATGAAACCCACA	3180
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Db	3562	GGCCGCACCATTTATTTGTCTACACACCCATGGACGAAGCTGACATCCTTGGGGACAGA	3621
Qy	3241	ATTGCCATCATCTCCCATGGGAAGCTGTGCTGTGTGGGCTCCTCCCTGTTTCTGAAGAAC	3300
Db	3622	ATTGCCATCATTTCCCATGGGAAGCTGTGTTGTGTGGGCTCCTCCCTGTTTCTGAAAAAC	3681
Qy	3301	CAGCTGGGAACAGGCTACTACCTGACCTTGGTCAAGAAAGATGTGGAATCCTCCCTCAGT	3360
Db	3682	CAGTTGGGAACGGGTTACTATCTGACCTGGTTAAGAAAGATGTGGAATCGTCCCTCAGT	3741
Qy	3361	TCCTGCAGAAAAGTAGTAGCACTGTGTCATACCTGAAAAAGGAGGACAGTGTTCCTCAG	3420
Db	3742	TCCTGCAGAAAAGTAGCAGCACCGTGTCTTGTCTGAAAAAGGAGGACAGTGTTCCTCAG	3800
Qy	3421	AGCAGTTCTGATGCTGGCCTGGGCAGCGACCATGAGAGTGACACGCTGACCATCGATGTC	3480
Db	3802	AGCAGTTCTGATGCTGGCCTGGGCAGCGACCATGAAAGTGACACGCTGACCATCGATGTC	3861
Qy	3481	TCTGCTATCTCCAACCTCATCAGGAAGCATGTGTCTGAAGCCCGGCTGGTGGAGACATA	3540
Db	3862	TCTGCTATCTCCAACCTCATCAGGAAGCAGTGTCTGAAGCCCGGCTGGTGGAGGACATT	3921
Qy	3541	GGGCATGAGCTGACCTATGTGCTGCCATATGAAGCTGCTAAGGAGGGAGCCTTTGTGGAA	3600
Db	3922	GGGCACGAGCTGACCTATGTGCTGCCGTAAGAAGCCGCGAAGGAGGGAGCCTTTGTGGAA	3981
Qy	3601	CTCTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTATGGCATCTCA	3660
Db	3982	CTCTTCCATGAGATTGATGACCGGCTCTCAGACCTGGGCATCTCCAGTTATGGCATCTCG	4041
Qy	3661	GAGACGACCTTGAAGAAAATATTCCTCAAGTGGCCGAAGAGAGTGGGGTGGATGCTGAG	3720
Db	4042	GAGACGACCTTGAAGAAAATATTCCTCAAGTGGCTGAAGAGAGCGGGGTGGATGCTGAG	4101
Qy	3721	ACCTCAGATGGTACCTTGCCAGCAAGACGAAACAGGCGGGCCTTCGGGGACAAGCAGAGC	3780
Db	4102	ACCTCAGATGGTACTTTGCCAGCAAGACGAAACAGACGGGCCTTCGGGGACAAGCAGAGC	4161
Qy	3781	TGTCTTCGCCCCGTTCACTGAAGATGATGCTGCTGATCCAAATGATTCTGACATAGACCCA	3840
Db	4162	TGTCTGCACCCATTTACGGAAGATGATGCTGTTGATCCCAATGACTCTGACATAGACCCA	4221
Qy	3841	GAATCCAGAGAGACAGACTTGCTCAGTGGGATGGATGGCAAAGGGTCTACCAGGTGAAA	3900
Db	4222	GAATCCAGGGAGACCGACCTGCTCAGTGGGATGGACGGCAAAGGCTCTACCAGCTGAAG	4281
Qy	3901	GGCTGGAAACTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAAGAGACTGCTAAATTGCC	3960
Db	4282	GGCTGGAAACTCACCCAGCAACAGTTTGTGGCCCTTTTGTGGAAGAGGCTGCTGATTGCC	4341
Qy	3961	AGACGGAGTCGGAAAGGATTTTTGTGCTCAGATTGTCTTGCCAGCTGTGTTTGTCTGCATT	4020
Db	4342	AGACGGAGCCGGAAGGGTTTCTTTGCTCAGATTGTCTTGCCAGCTGTCTTTGTTTGCATT	4401
Qy	4021	GCCCTTGTGTTTACGCTGATCGTGCCACCCCTTTGGCAAGTACCCAGCCTGGAACTTCAG	4080
Db	4402	GCCCTGGTCTTTCAGCTGATTGTGCCACCCCTTTGGCAAGTACCCAGCCTGGAACTTCAG	4461
Qy	4081	CCCTGGATGTATACCAAGAACAGTACACATTTGTGAGCAATGATGCTCCTGAGGACACGGGA	4140
Db	4462	CCCTGGATGTATATAGCAGTATACATTTGTGAGTAAATGATGCTCCCGAGGACATGGGC	4521
Qy	4141	ACCCTGGAACTCTTAAACGCCCTCACCAAAGACCCCTGGCTTCGGGACCCGCTGTATGGAA	4200
Db	4522	ACCAGGAACCTCTGAATGCTCTGACCAAAGATCCAGGCTTTGGGACCCGCTGTATGGAA	4581
Qy	4201	GGAAACCAATCCAGACACGCGCTGCCAGGACGGGAGGAAGAGTGGACCACTGCCCCCA	4260
Db	4582	GGAAACCAATCCAGATACCCCTTGCTTGGCTGGGAGGAGGAGTGGACCACTCAGCCCC	4641
Qy	4261	GTTCCTCCAGACCATCATGGACCTCTTCCAGAAATGGGAACTGGACAAATGCAGAACCTTCA	4320


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Db      4642  GTCCCCAGAGCATCGTGGACCTCTTCCAGAATGGAACTGGACCATGAAGAACCCCTCA 4701
Qy      4321  CCTGCATGCCAGTGTAGCAGCGACAAATCAAGAAGATGCTGCCTGTGTGTCCCCAGGG 4380
Db      4702  CCTGCGTGCCAGTGTAGCAGTGACAAATCAAGAAGATGCTGCCTGTGTGTCCCCAGGG 4761
Qy      4381  GCAGGGGGGCTGCCTCCTCCAC 4402
Db      4762  GCAGGGGGGCTGCCACCTCCTC 4783

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SEQ ID NO: 2

Result No.	Score	Query Match	Length	DB	ID	Description
1	11469	100.0	2201	21	AAV79380	Human ATP binding
2	11469	100.0	2201	22	AAE13021	Human ATP binding
3	11469	100.0	2201	22	AAM50227	Human ATP binding
4	11469	100.0	2201	23	ABP65164	Hypoxia-regulated
5	11469	100.0	2261	22	AAE13022	Human ATP binding
6	11469	100.0	2261	22	AAM50228	Human ATP binding
7	11469	100.0	2261	22	AAU02176	Human ABC1. Homo
8	11469	100.0	2261	22	AAU02177	Human ABC1 mutant
9	11469	100.0	2261	23	ABB83111	Human ABCA1 transp
10	11469	100.0	2261	23	ABP52092	Homo sapiens ABC t
11	11469	100.0	2261	23	AAE23000	Human ABC1 full-le
12	11468	100.0	2261	23	ABB83117	Polymorphic human
13	11468	100.0	2261	23	ABB83124	Polymorphic human
14	11466	100.0	2261	22	AAU02183	Human ABC1 mutant
15	11466	100.0	2261	22	AAU02188	Human ABC1 mutant
16	11466	100.0	2261	23	ABB83115	Polymorphic human
17	11466	100.0	2261	23	ABB83116	Polymorphic human
18	11466	100.0	2261	23	ABB83119	Polymorphic human
19	11466	100.0	2261	23	ABB83122	Polymorphic human
20	11466	100.0	2261	23	ABB83123	Polymorphic human
21	11465	100.0	2261	22	AAU02189	Human ABC1 mutant
22	11464	100.0	2261	23	ABB83121	Polymorphic human
23	11463	99.9	2261	22	AAU02181	Human ABC1 mutant
24	11462	99.9	2261	22	AAM78550	Human protein SEQ
25	11462	99.9	2263	22	ABB11956	Human ABCA1 homolo
26	11462	99.9	2263	22	AAM79534	Human protein SEQ
27	11461	99.9	2261	22	AAU02182	Human ABC1 mutant
28	11461	99.9	2261	22	AAU02186	Human ABC1 mutant
29	11459	99.9	2261	23	ABB83118	Polymorphic human
30	11458	99.9	2261	23	ABB83120	Polymorphic human
31	11440	99.7	2261	21	AAB38082	Human ABC1 cholest
32	11440	99.7	2261	22	AAB71749	Human ABC1 protein
33	11440	99.7	2261	24	ABU11899	Human ATP-binding
34	11439	99.7	2261	23	ABB81578	Human ABC-A-1-1 pr
35	11437	99.7	2261	21	AAB38109	Human ABC1 cholest
36	11437	99.7	2261	21	AAB38111	Human ABC1 cholest
37	11437	99.7	2261	21	AAB38114	Human ABC1 cholest
38	11437	99.7	2261	21	AAB38115	Human ABC1 cholest
39	11437	99.7	2261	21	AAB38117	Human ABC1 cholest

No.	Score	Match	Length	DB	ID	Description
1	6909	60.2	1375	3	US-08-665-259-26	Sequence 26, Appl
2	6909	60.2	1375	3	US-08-762-500-26	Sequence 26, Appl
3	3129.5	27.3	1457	3	US-08-665-259-27	Sequence 27, Appl
4	3129.5	27.3	1457	3	US-08-762-500-27	Sequence 27, Appl
5	2635.5	23.0	1684	3	US-08-665-259-25	Sequence 25, Appl
6	2635.5	23.0	1684	3	US-08-762-500-25	Sequence 25, Appl
7	2635.5	23.0	1704	3	US-08-762-500-75	Sequence 75, Appl

8	359	3.1	315	4	US-09-328-352-4388	Sequence 4388, Ap
9	354	3.1	332	4	US-09-107-532A-3752	Sequence 3752, Ap
10	352.5	3.1	335	4	US-09-252-991A-20837	Sequence 20837, A
11	352	3.1	322	4	US-09-107-532A-4662	Sequence 4662, Ap
12	346	3.0	589	4	US-09-328-352-7592	Sequence 7592, Ap
13	336.5	2.9	1280	2	US-08-583-276-19	Sequence 19, Appl
14	335.5	2.9	291	4	US-09-107-532A-4205	Sequence 4205, Ap
15	335.5	2.9	1280	4	US-09-767-594-2	Sequence 2, Appli
16	335.5	2.9	1280	6	5206352-4	Patent No. 5206352
17	333	2.9	1279	2	US-08-784-649A-2	Sequence 2, Appli
18	332	2.9	402	4	US-09-107-532A-5360	Sequence 5360, Ap
19	330.5	2.9	1280	2	US-08-752-447-2	Sequence 2, Appli

RESULT 1

US-08-665-259-26

; Sequence 26, Application US/08665259

; Patent No. 6028173

; GENERAL INFORMATION:

; APPLICANT: Landes, Gregory M.

; APPLICANT: Burn, Timothy C.

; APPLICANT: Connors, Timothy D.

; APPLICANT: Dackowski, William R.

; APPLICANT: Van Raay, Terence J.

; APPLICANT: Klinger, Katherine W.

; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,

; TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME

; NUMBER OF SEQUENCES: 73

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GENZYME CORPORATION

; STREET: One Mountain Road

; CITY: Framingham

; STATE: Massachusetts

; COUNTRY: United States of America

; ZIP: 01701

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/665,259

; FILING DATE: 17-JUN-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Dugan, Deborah A.

; REGISTRATION NUMBER: 37,315

; REFERENCE/DOCKET NUMBER: IG5-9.1

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; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1375 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

US-08-665-259-26

Query Match 60.2%; Score 6909; DB 3; Length 1375;

Best Local Similarity 96.9%; Pred. No. 0;

Matches 1332; Conservative 21; Mismatches 22; Indels 0; Gaps 0;

Qy 827 CMEEEPHTLKLGVSIQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSIL 886

Db 1 CMEEEPHTLRLGVSIQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSIL 60

Qy 887 TGLFPPTSGTAYILGKDIRSEMSTIRQNLGVCQHNVLFDMLTVEEHIWFYARLKGLSEK 946

Db	61	TGLFPPTSGTAYILGKDIRSEMSSIRQNLGVCPCQHNVLFDMLTVEEHIWFYARLKLGLSEK	120
Qy	947	HVKAEMEQMALDVGLPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPY	1006
Db	121	HVKAEMEQMALDVGLPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPY	180
Qy	1007	SRRGIWELLKLYRQGRITIIILSTHHMDEADVLDGRIAIISHGKLCCVGSSFLKNQLGTGY	1066
Db	181	SRRGIWELLKLYRQGRITIIILSTHHMDEADVLDGRIAIISHGKLCCVGSSFLKNQLGTGY	240
Qy	1067	YLTLVKKDVESSLSSCRNSSSTVSYLKKEDSVSQSSSDAGLGSDHESDTLTIDVSAISNL	1126
Db	241	YLTLVKKDVESSLSSCRNSSSTVSYLKKEDSVSQSSSDAGLGSDHESDTLTIDVSAISNL	300
Qy	1127	IRKHVSEARLVEDIGHELTYVLPYEAKEGAFVFLFHEIDDRLSDLGISSYGISETTLEE	1186
Db	301	IRKHVSEARLVEDIGHELTYVLPYEAKEGAFVFLFHEIDDRLSDLGISSYGISETTLEE	360
Qy	1187	IFLKVAEESGVDAETSDGTLPARNRRAFGDKQSCLRPFTEDDAADPNDSIDIPESRETD	1246
Db	361	IFLKVAEESGVDAETSDGTLPARNRRAFGDKQSCLRPFTEDDAADPNDSIDIPESRETD	420
Qy	1247	LLSGMDGKGSYQVKGWKL TQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSL	1306
Db	421	LLSGMDGKGSYQVKGWKL TQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSL	480
Qy	1307	IVPPFGKYP SLELQPWMYNEQYTFVSNDA PEDTGTLELLNALT KDPGFGTRCMEGNIPD	1366
Db	481	IVPPFGKYP SLELQPWMYNEQYTFVSNDA PEDMGTQELLNALT KDPGFGTRCMEGNIPD	540
Qy	1367	TPCQAGEEWTTPAVPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPPGAGGLPP	1426
Db	541	TPCLAGEEDWTISPVPQSI VDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPP	600
Qy	1427	PQRKQNTADILQDLTGRNIDSYLVKTYVQIIAKSLKNKIWNVEFRYGGFSLGVSNTQALP	1486
Db	601	PQRKQKTADILQNL TGRNIDSYLVKTYVQIIAKSLKNKIWNVEFRYGGFSLGVSNSQALP	660
Qy	1487	PSQEVNDATKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFL	1546
Db	661	PSHEVNDAIKQMKKLLKLT KDTSADRFLSSSLGRFMAGLDTKNNVKVWFNNKGWHAISSFL	720
Qy	1547	NVINNA I LRANLQKGENPSHYGITAFNHPLNLTKQQLSEVAPMTTSVDVLVSI C VIFAMS	1606
Db	721	NVINNA I LRANLQKGENPSQYGITAFNHPLNLTKQQLSEVALMTTSVDVLVSI C VIFAMS	780
Qy	1607	FVPASFVVFLIQERVS KAKHLQFISGVKPVIIYWLSNFVWDMCNYVVPATLVIIIFICFQQ	1666
Db	781	FVPASFVVFLIQERVS KAKHLQFISGVKPVIIYWLSNFVWDMCNYVVPATLVIIIFICFQQ	840
Qy	1667	KSYVSSTNLPVLALLLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNLFIGINGSVATF	1726
Db	841	KSYVSSTNLPVLALLLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNLFIGINGSVATF	900
Qy	1727	VLELFTDNKLNNDILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSW	1786
Db	901	VLELFTNNKLNNDILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSW	960
Qy	1787	DLVGRNLFAMAVEGVVFLITITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGG	1846
Db	961	DLVGRNLFAMAVEGVVFLITITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGG	1020
Qy	1847	GQNDILEIKELTKIYRRKRKPAVDRI CVGIPPEGCFLLGVNGAGKSTTFKMLTGDPTVT	1906
Db	1021	GQNDILEIKELTKIYRRKRKPAVDRI CIGIPPEGCFLLGVNGAGKSTTFKMLTGDPTVT	1080
Qy	1907	RGDAFLNRNLSILSNIHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKVGGE	1966
Db	1081	RGDAFLNKNSILSNIHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKVGGE	1140
Qy	1967	WAIRKLGVLKYGEKYAGNYSGGNKRKLSTAMALIGGPPVVFLEDEPTTGMDPKARRFLWNC	2026

```

Db      1141 WAIRKLGVLVYGEKYASNYSGGNKRKLSTAMALIGPPVVFLDEPTTGMDPKARRFLWNC 1200
Qy      2027 ALSVVKEGRSVVLTSHSMEECEALCTRMAIMVNGRFRCLGSVQHLEKRNFRGDTIVVRIA 2086
Db      1201 ALSIVKEGRSVVLTSHSMEECEALCTRMAIMVNGRFRCLGSVQHLEKRNFRGDTIVVRIA 1260
Qy      2087 GSNPDLKPVDFFGLAFPGSVPEKHRNMLQYQLPSSLSLARIFSILSQSKRLHIEDY 2146
Db      1261 GSNPDLKPVDFFGLAFPGSVLEKHRNMLQYQLPSSLSLARIFSILSQSKRLHIEDY 1320
Qy      2147 SVSQTTLQVFNFAKDQSDDDLKDLKSLHKNQTVVDVAVLTSFLQDEKVKESYV 2201
Db      1321 SVSQTTLQVFNFAKDQSDDDLKDLKSLHKNQTVVDVAVLTSFLQDEKVKESYV 1375

```

RESULT 2

US-08-762-500-26

; Sequence 26, Application US/08762500

; Patent No. 6030806

; GENERAL INFORMATION:

; APPLICANT: Landes, Gregory M.

; APPLICANT: Burn, Timothy C.

; APPLICANT: Connors, Timothy D.

; APPLICANT: Dackowski, William R.

; APPLICANT: Van Raay, Terence J.

; APPLICANT: Klinger, Katherine W.

; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,

; TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME

; NUMBER OF SEQUENCES: 83

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GENZYME CORPORATION

; STREET: One Mountain Road

; CITY: Framingham

; STATE: Massachusetts

; COUNTRY: United States of America

; ZIP: 01701

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/762,500

; FILING DATE: 09-DEC-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/665,259

; FILING DATE: 17-JUN-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/10469

; FILING DATE: 17-JUN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Dugan, Deborah A.

; REGISTRATION NUMBER: 37,315

; REFERENCE/DOCKET NUMBER: IG5-9.3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (508) 872-8400

; TELEFAX: (508) 872-5415

; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1375 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

US-08-762-500-26

Query Match

60.2%; Score 6909; DB 3; Length 1375;

Qy 1847 GQNDILEIKELTKIYRRKRKPAVDRICVGIPPGEFCGLLGVNGAGKSSTFKMLTGDITVT 1906
 |||:|||||:|||||
 Db 1021 GQNDILEIKELTKIYRRKRKPAVDRICIGIPPGEFCGLLGVNGAGKSTTFKMLTGDTPVT 1080

Qy 1907 RGDAFLNRNSILSNIHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKVG 1966
 |||:|||||:|||||
 Db 1081 RGDAFLNRNSILSNIHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKVG 1140

Qy 1967 WAIRKGLVKYGEKYAGNYSGGNKRKLSTAMALIGGPPVVFLDEPTTGMDPKARRFLWNC 2026
 |||:|||||:|||||
 Db 1141 WAIRKGLVKYGEKYAGNYSGGNKRKLSTAMALIGGPPVVFLDEPTTGMDPKARRFLWNC 1200

Qy 2027 ALSVVEGRSVVLTSHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNRFGDGYTIVVRIA 2086
 |||:|||||:|||||
 Db 1201 ALSIVVEGRSVVLTSHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNRFGDGYTIVVRIA 1260

Qy 2087 GSNPDLKPVQDFGLAFPGSVPEKHRNMLQYQLPSSLSSLARIFSILSQSKRLHIEDY 2146
 |||:|||||:|||||
 Db 1261 GSNPDLKPVQDFGLAFPGSVPEKHRNMLQYQLPSSLSSLARIFSILSQSKRLHIEDY 1320

Qy 2147 SVSQTTLQVFNFAKDQSDDDLKDLHLKQNTVVDVAVLTSFLQDEKVKESYV 2201
 |||:|||||:|||||
 Db 1321 SVSQTTLQVFNFAKDQSDDDLKDLHLKQNTVVDVAVLTSFLQDEKVKESYV 1375

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	10906	95.1	2201	2	A54774	ATP binding cassette
2	3338.5	29.1	1529	2	A59189	ATP-binding cassette
3	3129.5	27.3	1472	2	B54774	ATP binding cassette
4	2638.5	23.0	1704	2	S71363	probable ATP-binding
5	2635.5	23.0	1704	2	A59188	ATP-binding cassette
6	2061	18.0	1802	2	T33783	hypothetical prote
7	1975	17.2	1816	2	A84845	probable ABC trans
8	1854.5	16.2	1447	2	T15200	hypothetical prote
9	1792	15.6	1317	2	C88925	protein F33E11.4 [
10	1535.5	13.4	1758	2	F88559	protein C48B4.4b [
11	1528.5	13.3	1704	2	T42749	ATP-binding cassette
12	1526	13.3	1767	2	S60124	transport protein
13	1393	12.1	1246	2	T00826	hypothetical prote
14	1150.5	10.0	1564	2	T27121	hypothetical prote
15	1006.5	8.8	373	2	T47150	hypothetical prote
16	1005.5	8.8	1431	2	T22748	hypothetical prote
17	846	7.4	269	2	T46467	hypothetical prote
18	786.5	6.9	1011	2	T07712	probable ABC-type
19	695	6.1	900	2	T07717	probable ABC-type

RESULT 1

A54774

ATP binding cassette transporter ABC1 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 05-Apr-1995 #sequence_revision 05-Apr-1995 #text_change 02-Feb-2001

C;Accession: A54774

R;Luciani, M.F.; Denizot, F.; Savary, S.; Mattei, M.G.; Chimini, G.

Genomics 21, 150-159, 1994

A;Title: Cloning of two novel ABC transporters mapping on human chromosome 9.

A;Reference number: A54774; MUID:94375008; PMID:8088782

A;Accession: A54774

A;Molecule type: mRNA

A;Residues: 1-2201 <LUC>

A;Cross-references: GB:X75926; NID:g495256; PIDN:CAA53530.1; PID:g495257

C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

C;Keywords: ATP; duplication; nucleotide binding; P-loop

F;856-1047/Domain: ATP-binding cassette homology <ABC1>

F;873-880/Region: nucleotide-binding motif A (P-loop)

F:1869-2060/Domain: ATP-binding cassette homology <ABC2>
F:1886-1893/Region: nucleotide-binding motif A (P-loop)

Query Match 95.1%; Score 10906; DB 2; Length 2201;
Best Local Similarity 94.8%; Pred. No. 0;
Matches 2087; Conservative 54; Mismatches 60; Indels 0; Gaps 0;

Qy	1	MPSAGTLPWVQGIICNANNPCFRYPTEGEPAGVVGNFNKSIVSRFLSDARLLLYSQKDT	60
Db	1	MPSAGTLPWVQGIICNANNPCFRYPTEGEPAGVVGNFNKSIVSRFLSDAQRLLLYSQRDT	60
Qy	61	SMKDMRKVLRLTLQQIKKSSSNLKLQDFLVDNETFSGFLYHNLSLPKSTVDKMLRADVILH	120
Db	61	SIKDMHKVLRMLRQIKHPNSNLKLQDFLVDNETFSGFLQHNLSPRSTVDSLLQXNVGLQ	120
Qy	121	KVFLQGYQLHLTSLCNGSKSEEMIQLGDOEVSSEL CGLPREKLA AAEVRLSRNMDILKPIL	180
Db	121	KVFLQGYQLHLASLCNGSKLEEIQLGDAEVSALCGLPRKKLDAAEVRLRYNMDILKPVV	180
Qy	181	RTLNSTSPFPKELAEATKTLHLSGLTLAQELFSMRSWSDMRQEV MFLTNVNSSSSSTQI	240
Db	181	TKLNSTSHLPTQH LAEATTVLLDSLGLAQELFSTKSWSDMRQEV MFLTNVNSSSSSTQI	240
Qy	241	YQAVSRIVCGHPGGGLKIKSLNWEYEDNNYKALFGGNGTEEDAETFYDNSTTPYCNDLMK	300
Db	241	YQAVSRIVCGHPGGGLKIKSLNWEYEDNNYKALFGGNTEEDVDTFYDNSTTPYCNDLMK	300
Qy	301	NLESSPLSRIIWKALKPLLVGKILYTPDTPATRQVMAEVNKT FQELAVFHDLEGMWEELS	360
Db	301	NLESSPLSRIIWKALKPLLVGKILYTPDTPATRQVMAEVNKT FQELAVFHDLEGMWEELS	360
Qy	361	PKIWTFMENSQEMDLVRMLLDSRDNHFWEQQLDGLDWT AQDIVAFLAKHPEDVQSSNGS	420
Db	361	PQIWTFMENSQEMDLVRTLLDSRGNDQFWEQKLDGLDWT AQDIMAFLAKNPEDVQSPNGS	420
Qy	421	VYTWREAFNETNQAI RTISRFMECVNLNKLEPIATEVVLINKSMELLDERKFWAGIVFTG	480
Db	421	VYTWREAFNETNQAIQTISRFMECVNLNKLEPI TEVRLINKSMELLDERKFWAGIVFTG	480
Qy	481	ITPGSIELPHHVYKIRMDIDNVERTNKIKDGYWDPGPRADPFEDMRYVWGGFAYLQDVV	540
Db	481	ITPDSVELPHHVYKIRMDIDNVERTNKIKDGYWDPGPRADPFEDMRYVWGGFAYLQDVV	540
Qy	541	EQAIIRVLGTGEKKTGVYMQMPYPICYVDDIFLRVMSRSMPLFMTLAWIYSVAVIK GIV	600
Db	541	EQAIIRVLGTSEKKTGVYVQMPYPICYVDDIFLRVMSRSMPLFMTLAWIYSVAVIK SIV	600
Qy	601	YEKEARLKETMRIMGLDNSILWFSWFISSLIPLLVSAGLLV VILKGNLLPYSDPSVVFV	660
Db	601	YEKEARLKETMRIMGLDNGILWFSWFVSSLIPLLVSAGLLV VILKGNLLPYSDPSVVFV	660
Qy	661	FLSVFAVVTILQCFLISTLFSRANLAAACGGIIYFTLYLPYVLCVAWQDYVGFTLKFIFAS	720
Db	661	FLSVFAMVTILQCFLISTLFSRANLAAACGGIIYFTLYLPYVLCVAWQDYVGFSIKIFAS	720
Qy	721	LLSPVAFGFGCEYFALFEEQGIGVQWDNLFESPVEEDGFNLTTTSMMLFDFTFLYGVMTW	780
Db	721	LLSPVAFGFGCEYFALFEEQGIGVQWDNLFESPVEEDGFNLTTTAVSMMLFDFTFLYGVMTW	780
Qy	781	YIEAVFPGQYGI PRPWYFPCTKSYWFGEESEKSHPGSSNQKR ISEICMEEEPHTHLKLGVS	840
Db	781	YIEAVFPGQYGI PRPWYFPCTKSYWFGEEIDEKSHPGSSQKGVSEICMEEEPHTHLKLGVS	840
Qy	841	IQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTIMSILTGFPPTSGTAYIL	900
Db	841	IQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTIMSILTGFPPTSGTAYIL	900
Qy	901	GKDIRSEMSTIRQNLGVCPQHNVLFDMLTVEEBHIFWYARL KGLSEKHVKAEMEQMALDVG	960
Db	901	GKDIRSEMSSIRQNLGVCPQHNVLFDMLTVEEBHIFWYARL KGLSEKHVKAEMEQMALDVG	960

Qy	961	LPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYSRRGIWELLKYRQ	1020
Db	961	LPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYSRRGIWELLKYRQ	1020
Qy	1021	GRTIILSTHHMDEADVLDRIAIIISHGKLCCVGSSSLFLKNQLGTGYLTLVKKDVESSL	1080
Db	1021	GRTIILSTHHMDEADVLDRIAIIISHGKLCCVGSSSLFLKNQLGTGYLTLVKKDVESSL	1080
Qy	1081	SCRNSSSTVSYLKKEDSVSQSSSDAGLGSDESHTLTIDVSAISNLIRKHVSEARLVEDI	1140
Db	1081	SCRNSSSTVSYLKKEDSVSQSSSDAGLGSDESHTLTIDVSAISNLIRKHVSEARLVEDI	1140
Qy	1141	GHELTIVLPYEAAKEGAFVELFHEIDRLSDLGISYGISETTLEEFLKVAEESGVDAE	1200
Db	1141	GHELTIVLPYEAAKEGAFVELFHEIDRLSDLGISYGISETTLEEFLKVAEESGVDAE	1200
Qy	1201	TSDGTLPARRNRRAFGDKQSCLPFTEDDAADPNDSIDPESRETDLGSGMDGKGSYQVK	1260
Db	1201	TSDGTLPARRNRRAFGDKQSCLPFTEDDAADPNDSIDPESRETDLGSGMDGKGSYQVK	1260
Qy	1261	GWKLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSLIVPPFGKYPSELEQ	1320
Db	1261	GWKLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSLIVPPFGKYPSELEQ	1320
Qy	1321	PWMYNEQYTFVSNDAPEDTGTLELLNALT KDPGFGRTRCMEGNPIPDTPCQAGEEWTAP	1380
Db	1321	PWMYNEQYTFVSNDAPEDMGTQELNALT KDPGFGRTRCMEGNPIPDTPCLAGEEDWTISP	1380
Qy	1381	VPQTIMDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRKQNTADILQDL	1440
Db	1381	VPQSIQDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRKQNTADILQNL	1440
Qy	1441	TGRNISDYLVKTYVQIIAKSLKNKIWNENFRYGGFSLGVSNTQALPPSQEVNDATKQMKK	1500
Db	1441	TGRNISDYLVKTYVQIIAKSLKNKIWNENFRYGGFSLGVSNSQALPPSHEVNDAIKQMKK	1500
Qy	1501	HLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVINNAILRANLQK	1560
Db	1501	LLKLTKTDSADRFLSSLGRFMAGLDTKNNVKVWFNNKGWHAISSFLNVINNAILRANLQK	1560
Qy	1561	GENPSHYGITAFNHPLNLTQQLSEVAPMTTSVDVLVSICVIFAMSFVPASFVFLIQR	1620
Db	1561	GENPSQYGITAFNHPLNLTQQLSEVALMTTSVDVLVSICVIFAMSFVPASFVFLIQR	1620
Qy	1621	VSKAKHLQFISGVKPIYWLNSFVWDMCNYVVPATLVIIIFICFQKQSYVSSTNLPVLAL	1680
Db	1621	VSKAKHLQFISGVKPIYWLNSFVWDMCNYVVPATLVIIIFICFQKQSYVSSTNLPVLAL	1680
Qy	1681	LLLLYGSITPLMPASFVFKIPSTAYVVLTSVNLFIGINGSVATFVLELFTDNKLNNIN	1740
Db	1681	LLLLYGSITPLMPASFVFKIPSTAYVVLTSVNLFIGINGSVATFVLELFTNNKLNDIN	1740
Qy	1741	DILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSWDLVGRNLFAMAVEG	1800
Db	1741	DILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSWDLVGRNLFAMAVEG	1800
Qy	1801	VVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGGGQNDILEIKELTKI	1860
Db	1801	VVFFLITVLIQYRFFIRPRPVNAKLPPLNDEDEDVRRERQRILDGGGQNDILEIKELTKI	1860
Qy	1861	YRRKRKPAVDRICVGIPEGECFLLGVNGAGKSTTFKMLTGDTTVTRGDAFLNRNSILSN	1920
Db	1861	YRRKRKPAVDRICIGIPEGECFLLGVNGAGKSTTFKMLTGDTVPVTRGDAFLNKNLSILSN	1920
Qy	1921	IHEVHQNMGYCQFDAITELLTGREHVEFFALLRGVPEKEVGKVGWEAIRKGLVKYGEK	1980
Db	1921	IHEVHQNMGYCQFDAITELLTGREHVEFFALLRGVPEKEVGKVGWEAIRKGLVKYGEK	1980
Qy	1981	YAGNYSGGNKRKLSTAMALIGPPVVFLDEPTTGMDPKARRFLWNCALSIVKEGRSVVLT	2040
Db	1981	YASNYSGGNKRKLSTAMALIGPPVVFLDEPTTGMDPKARRFLWNCALSIVKEGRSVVLT	2040


```

Qy      2041 SHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNRFGDGYTIVVRIAGSNPDLKPVQDFFG 2100
        |||
Db      2041 SHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNRFGDGYTIVVRIAGSNPDLKPVQEFFG 2100

Qy      2101 LAFPGSVPEKEHRNMLQYQLPSSLSSLARIFSILSQSKRLHIEDYSVSQTTLDDQVFNF 2160
        |||
Db      2101 LAFPGSVLKEKHRNMLQYQLPSSLSSLARIFSILSQSKRLHIEDYSVSQTTLDDQVFNF 2160

Qy      2161 AKDQSDDDHLKDLKSLHKNQTVVDVAVLTSFLQDEKVKESYV 2201
        |||
Db      2161 AKDQSDDDHLKDLKSLHKNQTVVDVAVLTSFLQDEKVKESYV 2201

```

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	11466	100.0	2261	1	ABC1_HUMAN	O95477 homo sapien
2	10906	95.1	2261	1	ABC1_MOUSE	P41233 mus musculu
3	5689.5	49.6	2273	1	ABCR_HUMAN	P78363 homo sapien
4	4131	36.0	2436	1	ABC2_HUMAN	Q9bzc7 homo sapien
5	3989.5	34.8	2434	1	ABC2_MOUSE	P41234 mus musculu
6	2635.5	23.0	1704	1	ABC3_HUMAN	Q99758 homo sapien
7	1528.5	13.3	1704	1	CED7_CAEEL	P34358 caenorhabdi
8	411	3.6	330	1	DRRA_STRPE	P32010 streptomyce
9	380.5	3.3	343	1	NODI_RHISN	P55476 rhizobium s
10	366	3.2	304	1	NODI_RHIS3	P72335 rhizobium s
11	347	3.0	308	1	YADG_ECOLI	P36879 escherichia
12	347	3.0	335	1	NDI2_RHIME	Q8gnh6 rhizobium m
13	344.5	3.0	340	1	NODI_RHILO	P23703 rhizobium l
14	343.5	3.0	347	1	NODI_RHIGA	P50332 rhizobium g
15	335.5	2.9	1280	1	MDR1_HUMAN	P08183 homo sapien
16	331.5	2.9	355	1	NDI1_RHIME	O52618 rhizobium m
17	329.5	2.9	578	1	YBHF_ECOLI	P75776 escherichia
18	327	2.9	894	1	YHIH_ECOLI	P37624 escherichia
19	327	2.9	1276	1	MDR3_MOUSE	P21447 mus musculu

RESULT 2

ABC1_MOUSE

```

ID  ABC1_MOUSE      STANDARD;      PRT;  2261 AA.
AC  P41233;
DT  01-FEB-1995 (Rel. 31, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  15-SEP-2003 (Rel. 42, Last annotation update)
DE  ATP-binding cassette, sub-family A, member 1 (ATP-binding cassette
DE  transporter 1) (ATP-binding cassette 1) (ABC-1).
GN  ABCA1 OR ABC1.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=DBA/2; TISSUE=Macrophage;
RX  MEDLINE=94375008; PubMed=8088782;
RA  Luciani M.F., Denizot F., Savary S., Mattei M.-G., Chimini G.;
RT  "Cloning of two novel ABC transporters mapping on human chromosome
RT  9.";
RL  Genomics 21:150-159(1994).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=C57BL/6J;
RX  MEDLINE=21251004; PubMed=11352567;
RA  Qiu Y., Cavalier L., Chiu S., Yang X., Rubin E., Cheng J.-F.;
RT  "Human and mouse ABCA1 comparative sequencing and transgenesis

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RT studies revealing novel regulatory sequences.";

RL Genomics 73:66-76(2001).

CC -1- FUNCTION: CAMP-DEPENDENT AND SULFONYLUREA-SENSITIVE ANION

CC TRANSPORTER. KEY GATEKEEPER INFLUENCING INTRACELLULAR CHOLESTEROL

CC TRANSPORT (BY SIMILARITY).

CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN ADULT TISSUES. HIGHEST

CC LEVELS ARE FOUND IN PREGNANT UTERUS AND UTERUS.

CC -1- DOMAIN: MULTIFUNCTIONAL POLYPEPTIDE WITH TWO HOMOLOGOUS HALVES,

CC EACH CONTAINING AN HYDROPHOBIC MEMBRANE-ANCHORING DOMAIN AND AN

CC ATP BINDING CASSETTE (ABC) DOMAIN.

CC -1- PTM: Phosphorylation on Ser-2054 regulates phospholipid efflux (By

CC similarity).

CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCA SUBFAMILY.

CC -----

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DR EMBL; X75926; CAA53530.1; ALT_INIT.

DR EMBL; AF287263; AAG39073.1; ALT_INIT.

DR MGD; MGI:99607; Abcal.

DR GO; GO:0008203; P:cholesterol metabolism; IDA.

DR GO; GO:0030301; P:cholesterol transport; IDA.

DR InterPro; IPR003593; AAA_ATPase.

DR InterPro; IPR003439; ABC_transporter.

DR Pfam; PF00005; ABC_tran; 2.

DR ProDom; PD000006; ABC_transporter; 2.

DR SMART; SM00382; AAA; 2.

DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.

DR PROSITE; PS50893; ABC_TRANSPORTER_2; 2.

KW ATP-binding; Glycoprotein; Transmembrane; Transport; Phosphorylation.

FT	TRANSMEM	26	42	POTENTIAL.
FT	TRANSMEM	640	656	POTENTIAL.
FT	TRANSMEM	690	706	POTENTIAL.
FT	TRANSMEM	717	733	POTENTIAL.
FT	TRANSMEM	749	765	POTENTIAL.
FT	TRANSMEM	771	787	POTENTIAL.
FT	TRANSMEM	1041	1057	POTENTIAL.
FT	TRANSMEM	1351	1367	POTENTIAL.
FT	TRANSMEM	1661	1677	POTENTIAL.
FT	TRANSMEM	1708	1724	POTENTIAL.
FT	TRANSMEM	1737	1753	POTENTIAL.
FT	TRANSMEM	1775	1791	POTENTIAL.
FT	TRANSMEM	1854	1870	POTENTIAL.
FT	NP_BIND	933	940	ATP (POTENTIAL).
FT	NP_BIND	1946	1953	ATP (POTENTIAL).
FT	MOD_RES	1042	1042	PHOSPHORYLATION (BY PKA) (MAJOR) (BY
FT				SIMILARITY).
FT	MOD_RES	2054	2054	PHOSPHORYLATION (BY PKA) (MAJOR) (BY
FT				SIMILARITY).
FT	CARBOHYD	14	14	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	98	98	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	151	151	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	161	161	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	196	196	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	244	244	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	292	292	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	337	337	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	349	349	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	400	400	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	478	478	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	489	489	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	521	521	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	820	820	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1144	1144	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1294	1294	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1453	1453	N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1499 1499 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1504 1504 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1637 1637 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2044 2044 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2238 2238 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 1567 1568 MISSING (IN REF. 2).
 FT CONFLICT 2024 2024 MISSING (IN REF. 2).
 SQ SEQUENCE 2261 AA; 254011 MW; FAE62B21FD1D09F9 CRC64;

Query Match 95.1%; Score 10906; DB 1; Length 2261;
 Best Local Similarity 94.8%; Pred. No. 0;
 Matches 2087; Conservative 54; Mismatches 60; Indels 0; Gaps 0;

Qy 1 MPSAGTLPWVGQIICNANNPCFRYPTPGEAPGVVGNFNKSIVARLFSADARLLLYSQKDT 60
 Db 61 MPSAGTLPWVGQIICNANNPCFRYPTPGEAPGVVGNFNKSIVSRLFSDAQRLLYSQKDT 120
 Qy 61 SMKDMRKVLRTLQKIKSSSNLKLQDFLVDNETFSGFLYHNLSPKSTVDKMLRADVILH 120
 Db 121 SIKDMHKVLRMLRQIKHPNSNLKLQDFLVDNETFSGFLQHNLSLPRSTVDSLQXNVGLQ 180
 Qy 121 KVFLQGYQLHLTSLCNGSKSEMIQLGDQEVSELGCLPREKLAARVLRNMDILKPIL 180
 Db 181 KVFLQGYQLHLASLCNGSKLEBIIQLGDAEVSALCGLPRKKLDAARVLRNMDILKPVV 240
 Qy 181 RTLNSTSPFPKELAEATKTLHSLGLTLAGELFSMRWSMDRQEVFMFLTNVNSSSSSTQI 240
 Db 241 TKLNSTSHLPTQHLAEATTVLLDSLGLLAGELFSTKSWSDMRQEVFMFLTNVNSSSSSTQI 300
 Qy 241 YQAVSRIVCGHPEGGLKIKSLNWEYEDNNYKALFGGNGTEEDAETFYDNSTTPYCNDLMK 300
 Db 301 YQAVSRIVCGHPEGGLKIKSLNWEYEDNNYKALFGGNTEEDVDTFYDNSTTPYCNDLMK 360
 Qy 301 NLESSPLSRIIWKALKPLLVGKILYTPDTPATRQVMAEVNKTQELAVFHDLEGMWEELS 360
 Db 361 NLESSPLSRIIWKALKPLLVGKILYTPDTPATRQVMAEVNKTQELAVFHDLEGMWEELS 420
 Qy 361 PKIWTFMENSQEMDLVRMLLDSRDNDHFWEQQLDGLDWTQAQDIVAFLAKHPEDVQSSNGS 420
 Db 421 PQIWTFMENSQEMDLVRTLLDSRGNDQFWEQKLDGLDWTQAQDIMAFLAKNPEDVQSPNGS 480
 Qy 421 VYTWREAFNETNQAIQITISRFMECVNLNLEPIATEVWLINKSMELDERKFWAGIVFTG 480
 Db 481 VYTWREAFNETNQAIQITISRFMECVNLNLEPIATEVWLINKSMELDERKFWAGIVFTG 540
 Qy 481 ITPGSIELPHHVYKIRMDIDNVERTNKIKDGYWDPGPRADPFEDMRYVWGGFAYLQDVV 540
 Db 541 ITPDSVELPHHVYKIRMDIDNVERTNKIKDGYWDPGPRADPFEDMRYVWGGFAYLQDVV 600
 Qy 541 EQAIIRVLTGTEKKTGVYVQMPYPCYVDDIFLRVMSRSMPLFMTLAWIYSVAVIIKIV 600
 Db 601 EQAIIRVLTGSEKKTGVYVQMPYPCYVDDIFLRVMSRSMPLFMTLAWIYSVAVIISIV 660
 Qy 601 YEKEARLKETMRIMGLDNSILWFSWFISSLIPLLVSAAGLLVVLKGNLLPYSDPSVVFV 660
 Db 661 YEKEARLKETMRIMGLDNGILWFSWFISSLIPLLVSAAGLLVVLKGNLLPYSDPSVVFV 720
 Qy 661 FLSVFAVVTILQCFLISTLFSRANLAAACGGIIYFTLYLPYVLCVAWQDYVGFTLKIFAS 720
 Db 721 FLSVFAVVTILQCFLISTLFSRANLAAACGGIIYFTLYLPYVLCVAWQDYVGFSIKIFAS 780
 Qy 721 LLSPVAFGFGCEYFALFEEQIGVQWDLNLFESPVEEDGFNLTTSVSMMLFDFTLYGVMTW 780
 Db 781 LLSPVAFGFGCEYFALFEEQIGVQWDLNLFESPVEEDGFNLTTAVSMMLFDFTLYGVMTW 840
 Qy 781 YIEAVFPGQYGIIPRPWYFPCTKSYWFGESDEKSHPGSNQKRISICMEEEPHTHLKLGVS 840
 Db 841 YIEAVFPGQYGIIPRPWYFPCTKSYWFGEEIDEKSHPGSSQKGVSEICMEEEPHTHLRLGVS 900
 Qy 841 IQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYIL 900

Db 901 IQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYIL 960
 Qy 901 GKDIRSEMSTIRQNLGVCPQHNVLFDMLTVEEHIWIFYARLKGLSEKHVKAEMEOMALDVG 960
 Db 961 GKDIRSEMSSIRQNLGVCPQHNVLFDMLTVEEHIWIFYARLKGLSEKHVKAEMEOMALDVG 1020
 Qy 961 LPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVLDEPTAGVDPYSRRGIWELLKRYQ 1020
 Db 1021 LPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVLDEPTAGVDPYSRRGIWELLKRYQ 1080
 Qy 1021 GRTIILSTHHMDEADVLDRIAIIISHGKLCCVGSSFLKNQLGTGYLTLVKKDVESSL 1080
 Db 1081 GRTIILSTHHMDEADILGRIAIIISHGKLCCVGSSFLKNQLGTGYLTLVKKDVESSL 1140
 Qy 1081 SCRNSSTVSYLKKEDSVSQSSDAGLGSDESHTLTIDVSAISNLIRKXVSEARLVEDI 1140
 Db 1141 SCRNSSTVSCLKKEDSVSQSSDAGLGSDESHTLTIDVSAISNLIRKXVSEARLVEDI 1200
 Qy 1141 GHELTIVLPYEAAKEGAFVELFHEIDRLSDLGISSYGISETTLEEIFLKVAEESGVDAE 1200
 Db 1201 GHELTIVLPYEAAKEGAFVELFHEIDRLSDLGISSYGISETTLEEIFLKVAEESGVDAE 1260
 Qy 1201 TSDGTLFARRNRRAFGDKQSLRPFTEDDAADPNDSIDIPESRETDLGMDGKGSYQVK 1260
 Db 1261 TSDGTLFARRNRRAFGDKQSLHPFTEDDAADPNDSIDIPESRETDLGMDGKGSYQVK 1320
 Qy 1261 GWKLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSILVPPFGKYPSELEQ 1320
 Db 1321 GWKLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSILVPPFGKYPSELEQ 1380
 Qy 1321 PWMYNEQYTFVSNDAPEDTGTLELLNALT KDPGFGTRCMEGNPIPDTPCQAGEEWTAP 1380
 Db 1381 PWMYNEQYTFVSNDAPEDMGTQELLNALT KDPGFGTRCMEGNPIPDTPCLAGEEDWTISP 1440
 Qy 1381 VPQTIMDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRKQNTADILQDL 1440
 Db 1441 VPQSIQDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRKQNTADILQNL 1500
 Qy 1441 TGRNISDYLVKTYVQIIAKSLKNKIWNNEFRYGGFSLGVSNTQALPPSQEVNDATKQMKK 1500
 Db 1501 TGRNISDYLVKTYVQIIAKSLKNKIWNNEFRYGGFSLGVSNSQALPPSHEVNDAIKQMKK 1560
 Qy 1501 HLKLAADSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVINNAILRANLQK 1560
 Db 1561 LLKLTQDTSADRFLSSLGRFMAGLDTKNNVKVWFNNKGWHAISSFLNVINNAILRANLQK 1620
 Qy 1561 GENPSHYGITAFNHPLNLTQQLSEVAPMTTSVDVLVSICVIFAMSFVPASFVFLIQR 1620
 Db 1621 GENPSQYGITAFNHPLNLTQQLSEVALMTTSVDVLVSICVIFAMSFVPASFVFLIQR 1680
 Qy 1621 VSKAKHLQFISGVKPIYWLNSFVWDMCNYPVATLVIIIFICFQKQSYVSSTNLPVLAL 1680
 Db 1681 VSKAKHLQFISGVKPIYWLNSFVWDMCNYPVATLVIIIFICFQKQSYVSSTNLPVLAL 1740
 Qy 1681 LLLLYGWSITPLMPASFVFKIPSTAYVVLTSVNLFIGINGSVATFVLELFTDNKLNNIN 1740
 Db 1741 LLLLYGWSITPLMPASFVFKIPSTAYVVLTSVNLFIGINGSVATFVLELFTNNKLNDIN 1800
 Qy 1741 DILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSWDLVGRNLFAMAVEG 1800
 Db 1801 DILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSWDLVGRNLFAMAVEG 1860
 Qy 1801 VVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGGGQNDILEIKELTKI 1860
 Db 1861 VVFFLITVLIQYRFFIRPRPVNAKLPPLNDEDEDVRRERQRILDGGGQNDILEIKELTKI 1920
 Qy 1861 YRRKRKPAVDRIICVIPPGECPGLLGVNGAGKSTTFKMLTGDTPTVTRGDAFLNKNLSILN 1920
 Db 1921 YRRKRKPAVDRIICVIPPGECPGLLGVNGAGKSTTFKMLTGDTPTVTRGDAFLNKNLSILN 1980
 Qy 1921 IHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKVGWNAIRKGLGVKYEK 1980

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Db      1981  |||||||||||||||||||||||||||||||||||||||| 2040
Qy      1981  YAGNYSGGNKRKLSTAMALIGGPPVVFLDEPTTGMDPKARRFLWNCALSVVKEGRSVVLT 2040
Db      2041  || ||||||||||||||||||||||||||||||||||||:|||||||
Qy      2041  SHSMEECEALCTRMALMVNGRFRCLGSVQHLKNRFGDGYTIVVRIAGSNPDLKPVQDFFG 2100
Db      2101  ||||||||||||||||||||||||||||||||||||:|||
Qy      2101  LAFPGSVPKEKHRNMLQYQLPSSLSSLARIFSILSQSKRLHIEDYSVSQTTLDQVFNF 2160
Db      2161  |||||| |||||||||||||||||||||||||||||||||||
Qy      2161  LAFPGSVLKEKHRNMLQYQLPSSLSSLARIFSILSQSKRLHIEDYSVSQTTLDQVFNF 2220
Db      2161  AKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQDEKVKEYSV 2201
Db      2221  |||||||||||||||||||||||||||||
Db      2221  AKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQDEKVKEYSV 2261

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